This listing of claims will replace all prior versions, and listings, of claims, in the application:

LISTING OF CLAIMS:

Claims 1-22 (cancelled)

Claim 23 (currently amended) A method comprising:

(a) digesting separately nucleic acids from a mixture of at least two nucleic acid populations with at least one restriction enzyme;

(b) ligating a[n] blunt ended adaptor sequence to the restriction fragments resulting from the digestion in step (a);

(c) amplifying adaptor-ligated restriction fragments generated in step (b) using an adaptor-specific primer to produce amplification products having different ends in respect to each population;

(d) hybridizing the amplification products of step (c) from the different nucleic acid populations with each other to generate a mixture comprising homoduplexes and heteroduplexes;

(e) eliminating blunt ended homoduplexes from heteroduplexes having forked ends by digesting the homoduplexes with an enzyme that specifically digests blunt ended double-stranded DNA fragments;

(f) eliminating mismatched heteroduplexes by using mismatch repair enzymes; and

(g) identifying, isolating or separating fully-matched heteroduplexes, thereby identifying, isolating or separating nucleic acid fragments that are identical between said at least two nucleic acid populations.

Claim 24 (previously presented) The method of claim 23, wherein said nucleic acid populations comprise genomic DNA populations.

Claim 25(previously presented) The method of claim 24, wherein said nucleic acid populations comprise human genomic DNA populations.

Claim 26 (previously presented) The method of claim 25, wherein said nucleic acid populations comprise nucleic acid populations from different subjects having a common trait of interest.

Claim 27 (previously presented) The method of claim 23, wherein said nucleic acid populations comprise one or more selected chromosomes.

Claim 28 (previously presented) The method of claim 23, wherein said nucleic acid populations comprise nucleic acid populations from different sources.

Claim 29 (previously presented) The method of claim 23, wherein said restriction fragments are size-selected prior to said amplifying step.

Claims 30-31 (cancelled)

Claim 32 (previously presented) The method of claim 23, wherein said adaptor sequence comprises a 5 base to 100 base long double-stranded DNA fragment.

Claim 33 (cancelled)

Claim 34 (previously presented) The method of claim 23, wherein said amplifying step further comprises using a polymerase chain reaction technique.

Claim 35 (cancelled)

Claim 36 (previously presented) The method of claim 23, wherein said primer is labelled by a technique selected from the group consisting of (a) adding a unique 5'-sequence to the primer; (b) adding a chemical activity to the primer; and (c) adding modified nucleotides into the primer, allowing one to distinguish between or among the amplification products from the nucleic acids of said at least two populations.

Claims 37-38 (cancelled)

Claim 39 (previously presented) The method of claim 23, wherein said eliminating step (f) comprises incubating the hybridization mixture of step (d) with MutS, MutL, and MutH, resulting in a specific cleavage of mismatched heteroduplexes.

Claims 40-45 (cancelled)

Claim 46 (withdrawn) A kit suitable for genetic analysis according to the method of claim 23, comprising:

(a) a double stranded adaptor molecule; and

(b) a specific, labeled primer.

Claim 47 (withdrawn) The kit of claim 46, further comprising control deoxyribonucleic acids.

Claim 48 (withdrawn) The kit of claim 46, further comprising a means for the detection of selected DNA fragments.

Claim 49 (withdrawn) The kit of claim 46, further comprising a means for the detection of selected DNA fragments.

Claim 50 (withdrawn) The kit of claim 49, wherein said means comprises an ordered DNA array.

Claim 51 (withdrawn) The kit of claim 49, wherein said means comprises coded beads carrying specific DNA sequences.

Claim 52 (withdrawn) A method of separating identical DNA fragments from complex mixtures of at least two nucleic acid populations, comprising:

(a) hybridizing the populations; and

(b) separating the fully-matched heterohybrids formed via the hybridization;

wherein said nucleic acid populations comprise amplified nucleic acids.

Claim 53 (withdrawn) A method of identifying DNA regions that are relevant to a pathological condition or a particular trait, comprising:

(a) hybridizing at least two nucleic acid populations from different sources having the particular trait or pathology; and

(b) separating the fully-matched heterohybrids formed which contain DNA regions that are relevant to said pathological condition or particular trait;

wherein said nucleic acid populations are chosen from the group consisting of amplified nucleic acids and pre-selected nucleic acids.

Claim 54 (previously presented) The method of claim 23, wherein the enzyme that specifically digests blunt ended double-stranded DNA fragments is exonuclease III.

Claim 55 (previously presented) The method of claim 23, wherein the method further comprises after step (e) a step of eliminating newly created single strands.

Claim 56 (previously presented) The method of claim 55, wherein said step of eliminating newly created single strands comprises binding said created single strands to a single strand specific matrix.